FULL LENGTH APO-A1 SEQUENCE

1
MKAAVLTLAVLFLTGSQARHFWQQDEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE

TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE
194
LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHA
267
KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ (SEQ ID NO:2)

sig_peptide 20..91
mature protein 92..820

20 a tgaaagetge ggtgetgace ttggeegtge tetteetgae

61 ggggagccag geteggcatt tetggeagca agatgaacce ceccagagce cetgggateg

121 agtgaaggae etggecaetg tgtacgtgga tgtgeteaaa gacageggea gagactatgt

181 gteccagttt gaaggeteeg eettgggaaa acagetaaac etaaagetee ttgacaactg

241 ggacagegtg acetecaect teagcaaget gegegaacag eteggeeetg tgacceagga

301 gttetgggat aacetggaaa aggagacaga gggeetgagg eaggagatga geaaggatet

361 ggaggaggtg aaggeeaagg tgcageeeta eetggaegae ttecagaaga agtggeagga

421 ggagatggag etetacegee agaaggtgga geegetgege geagagetee aagagggege

481 gegeeagaag etgcacgage tgcaagagaa getgageeea etgggegagg agatgegea

541 eegegegege geeeatgtgg aegegetgeg eaegeatetg geeeeetaca gegaegget

601 gegeeagege ttggeegee geettgagge teteaaggag aaeggegege

601 gegeeagege ttggeegee geettgagge teteaaggag aaeggegege eagaetgge

721 getegaggae eteegeeaag geetgetgee egtgetggag agetteaagg teagetteet

781 gagegetete gaggagtaea etaagaaget eaaeaeceag (SEQ ID NO:1)

FIG. 1A

18K N-TERMINAL FRAGMENT

25 DEPPQSPWDRVKDLATVYVD

601 g (SEQ ID NO:4)

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVEPLRAELQEGARQKLHE 194 LQEKLSPLGEEMRDRARAHVDALRTHLAPYSDEL (SEQ ID NO:3)

- 92 gatgaaccc ccccagagcc cctgggatcg
- agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg ggacagcgtg acctccacct tcagcaagct gcgcgaacag ctcggccctg tgacccagga 301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga 421 ggagatggag ctctaccgcc agaaggtgga gccgctgcgc gcagagctcc aagagggcgc 481 gcgccagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gcccctaca gcgacgagct

FIG. 1B

13K N-TERMINAL FRAGMENT

25 DEPPQSPWDRVKDLATVYVD

VLKDSGRDYVSQFEGSALGKQLNLKLLDNWDSVTSTFSKLREQLGPVTQEFWDNLEKE 144 TEGLRQEMSKDLEEVKAKVQPYLDDFQKKWQEEMELYRQKVE (PORTION OF SEQ ID NO:3)

- 92 gatgaaccc ccccagagcc cctgggatcg
- 121 agtgaaggac ctggccactg tgtacgtgga tgtgctcaaa gacagcggca gagactatgt
- 181 gtcccagttt gaaggctccg ccttgggaaa acagctaaac ctaaagctcc ttgacaactg
- 241 ggacagegtg acetecacet teageaaget gegegaacag eteggeeetg tgaceeagga
- 301 gttctgggat aacctggaaa aggagacaga gggcctgagg caggagatga gcaaggatct
- 361 ggaggaggtg aaggccaagg tgcagcccta cctggacgac ttccagaaga agtggcagga
- 421 ggagatggag ctctaccgcc agaaggtgga g (PORTION OF SEQ ID NO:4)

13K C-TERMINAL FRAGMENT

156 QKLHE

194 LQEKLSPLGEEMRD RARAHVDALRTHLAPYSDELRQRLAARLEALKENGGARLAEYHA 267 KATEHLSTLSEKAKPALEDLRQGLLPVLESFKVSFLSALEEYTKKLNTQ (PORTION OF SEQ ID NO:2)

cagaag ctgcacgagc tgcaagagaa gctgagccca ctgggcgagg agatgcgcga
ccgcgcgcgc gcccatgtgg acgcgctgcg cacgcatctg gccccctaca gcgacgagct
gcgccagcgc ttggccgcgc gccttgaggc tctcaaggag aacggcggcg ccagactggc
cgagtaccac gccaaggcca ccgagcatct gagcacgctc agcgagaagg ccaagcccgc
gctcgaggac ctccgccaag gcctgctgcc cgtgctggag agcttcaagg tcagcttcct
gagcgctctc gaggagtaca ctaagaagct caacacccag (PORTION OF SEQ ID NO:1)